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 McBride, Jere W.
 Yu, Xue-Jie

<120> Homologous 28-Kilodalton Immunodominant Protein
 Genes of *Ehrlichia canis* and Uses Thereof

<130> D6152CIP2/D/D1

<141> 2003-12-09

<150> 09/811,007
 <151> 2003-03-16

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<220>
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gacgcgcaca	ggtactgcgc	tctatctcat	cacacatcgg	cagccatgga	600
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<213>     Ehrlichia canis

<220>
<223>     amino acid sequence of E. canis p28-7 protein

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Pro	Ile	Leu	Lys	Asn	Lys	His	Ala	Asp	Phe	Thr	Val	Pro	Asn	Tyr	80	85	90
Ser	Phe	Arg	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala	95	100	105
Ile	Gly	Tyr	Ser	Met	Gly	Gly	Pro	Arg	Ile	Glu	Phe	Glu	Ile	Ser	110	115	120
Tyr	Glu	Ala	Phe	Asp	Val	Lys	Ser	Pro	Asn	Ile	Asn	Tyr	Gln	Asn	125	130	135
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Leu	Ile	Ser	Met	Phe	Glu	Ala	Thr	Ser	Pro	Lys	Ile	Ser	Tyr	Gln	200	205	210
Gly	Lys	Leu	Gly	Ile	Ser	Tyr	Ser	Ile	Asn	Pro	Glu	Thr	Ser	Val	215	220	225
Phe	Ile	Gly	Gly	His	Phe	His	Arg	Ile	Ile	Gly	Asn	Glu	Phe	Arg	230	235	240
Asp	Ile	Pro	Ala	Ile	Val	Pro	Ser	Asn	Ser	Thr	Thr	Ile	Ser	Gly	245	250	255
Pro	Gln	Phe	Ala	Thr	Val	Thr	Leu	Asn	Val	Cys	His	Phe	Gly	Leu	260	265	270
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<220>
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Ser	Val	Pro	His	Phe	Gly	Ile	Phe	Ser	Ala	Glu	Glu	Glu	Lys	Lys		
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Ala	Ile	Ser	Ser	Gln	Ser	Pro	Asp	Asp	Asn	Phe	Thr	Ile	Arg	Asn		
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Tyr	Ser	Phe	Lys	Tyr	Ala	Ser	Asn	Lys	Phe	Leu	Gly	Phe	Ala	Val		
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Glu	Thr	Ala	Ser	Lys	Asn	Ile	Pro	Leu	Ser	Pro	Tyr	Ile	Cys	Ala		
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Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ala	Tyr	Phe	Val	Ser		
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				230					235					240		
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Asp	Glu	Ile	Val	Gly	Pro	Gln	Phe	Ala	Thr	Val	Thr	Leu	Asn	Val
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 Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
 95 100 105
 Ile Gly Tyr Ser Met Gly Gly Pro Arg Ile Glu Leu Glu Val Leu
 110 115 120
 Tyr Glu Thr Phe Asp Val Lys Asn Gln Asn Asn Asn Tyr Lys Asn
 125 130 135
 Gly Ala His Arg Tyr Cys Ala Leu Ser His His Ser Ser Ala Thr
 140 145 150
 Ser Met Ser Ser Ala Ser Asn Lys Phe Val Phe Leu Lys Asn Glu
 155 160 165
 Gly Leu Ile Asp Leu Ser Phe Met Ile Asn Ala Cys Tyr Asp Ile
 170 175 180
 Ile Ile Glu Gly Met Pro Phe Ser Pro Tyr Ile Cys Ala Gly Val
 185 190 195

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Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Gly	Tyr	Ser	Ile	Ser	Ser	Glu
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Ala	Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Arg	Val	Ile	Gly	Asn
				230					235					240
Glu	Phe	Arg	Asp	Ile	Pro	Ala	Met	Val	Pro	Ser	Gly	Ser	Asn	Leu
				245					250					255
Pro	Glu	Asn	Gln	Phe	Ala	Ile	Val	Thr	Leu	Asn	Val	Cys	His	Phe
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 <213> *Ehrlichia canis*

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Lys	Thr	Thr	Val	Val	Tyr	Gly	Leu	Lys	Glu	Asn	Trp	Ala	Gly	Asp
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Ala	Ile	Ser	Ser	Gln	Ser	Pro	Asp	Asp	Asn	Phe	Thr	Ile	Arg	Asn
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Tyr	Ser	Phe	Lys	Tyr	Ala	Ser	Asn	Lys	Phe	Leu	Gly	Phe	Ala	Val
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Ala	Ile	Gly	Tyr	Ser	Ile	Gly	Ser	Pro	Arg	Ile	Glu	Val	Glu	Met
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 <213> *Ehrlichia canis*

<220>
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Ala	Ser	His	Phe	Gly	Ile	Phe	Ser	Ala	Lys	Glu	Glu	Gln	Ser	Phe
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Thr	Lys	Val	Leu	Val	Gly	Leu	Asp	Gln	Arg	Leu	Ser	His	Asn	Ile
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Ile	Asn	Asn	Asn	Asp	Thr	Ala	Lys	Ser	Leu	Lys	Val	Gln	Asn	Tyr
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Ser	Phe	Lys	Tyr	Lys	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala
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Ile	Gly	Tyr	Ser	Ile	Gly	Asn	Ser	Arg	Ile	Glu	Leu	Glu	Val	Ser
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His	Glu	Ile	Phe	Asp	Thr	Lys	Asn	Pro	Gly	Asn	Asn	Tyr	Leu	Asn
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Ser	Asp	Gly	Asn	Ser	Gly	Asp	Trp	Tyr	Thr	Ala	Lys	Thr	Asp	Lys	
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Phe	Val	Leu	Leu	Lys	Asn	Glu	Gly	Leu	Leu	Asp	Val	Ser	Phe	Met	
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Leu	Asn	Ala	Cys	Tyr	Asp	Ile	Thr	Thr	Glu	Lys	Met	Pro	Phe	Ser	
				185					190					195	
Pro	Tyr	Ile	Cys	Ala	Gly	Ile	Gly	Thr	Asp	Leu	Ile	Ser	Met	Phe	
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Glu	Thr	Thr	Gln	Asn	Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	
				215					220					225	
Asn	Tyr	Thr	Ile	Asn	Ser	Arg	Val	Ser	Val	Phe	Ala	Gly	Gly	His	
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Phe	His	Lys	Val	Ile	Gly	Asn	Glu	Phe	Lys	Gly	Ile	Pro	Thr	Leu	
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Leu	Pro	Asp	Gly	Ser	Asn	Ile	Lys	Val	Gln	Gln	Ser	Ala	Thr	Val	
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<212> PRT

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* P28

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Ala	Ser	His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Glu	Glu	Arg	Asn	Thr	50	55	60
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Ile	Gly	Tyr	Ser	Met	Asp	Gly	Pro	Arg	Ile	Glu	Leu	Glu	Val	Ser	110	115	120
Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn	Gln	Gly	Asn	Asn	Tyr	Lys	Asn	125	130	135
Glu	Ala	His	Arg	Tyr	Cys	Ala	Leu	Ser	His	Asn	Ser	Ala	Ala	Asp	140	145	150
Met	Ser	Ser	Ala	Ser	Asn	Asn	Phe	Val	Phe	Leu	Lys	Asn	Glu	Gly	155	160	165
Leu	Leu	Asp	Ile	Ser	Phe	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Val	Val	170	175	180
Gly	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Ile	Gly	185	190	195
Thr	Asp	Leu	Val	Ser	Met	Phe	Glu	Ala	Thr	Asn	Pro	Lys	Ile	Ser	200	205	210
Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Ser	Pro	Glu	Ala	215	220	225
Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile	Gly	Asn	Glu	230	235	240
Phe	Arg	Asp	Ile	Pro	Thr	Ile	Ile	Pro	Thr	Gly	Ser	Thr	Leu	Ala	245	250	255
Gly	Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Ile	Leu	Asp	Val	Cys	His	260	265	270

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<210> 10

<211> 283

<212> PRT

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* OMP-1B

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Asn	Asp	Thr	Gly	Ile	Asn	Asp	Ser	Arg	Glu	Gly	Phe	Tyr	Ile	Ser	35	40	45
Val	Lys	Tyr	Asn	Pro	Ser	Ile	Ser	His	Phe	Arg	Lys	Phe	Ser	Ala	50	55	60
Glu	Glu	Ala	Pro	Ile	Asn	Gly	Asn	Thr	Ser	Ile	Thr	Lys	Lys	Val	65	70	75
Phe	Gly	Leu	Lys	Lys	Asp	Gly	Asp	Ile	Ala	Gln	Ser	Ala	Asn	Phe	80	85	90
Asn	Arg	Thr	Asp	Pro	Ala	Leu	Glu	Phe	Gln	Asn	Asn	Leu	Ile	Ser	95	100	105
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Glu	Leu	Glu	Ala	Ala	Tyr	Gln	Lys	Phe	Asp	Ala	Lys	Asn	Pro	Asp	125	130	135
Asn	Asn	Asp	Thr	Asn	Ser	Gly	Asp	Tyr	Tyr	Lys	Tyr	Phe	Gly	Leu	140	145	150
Ser	Arg	Glu	Asp	Ala	Ile	Ala	Asp	Lys	Lys	Tyr	Val	Val	Leu	Lys	155	160	165

Asn	Glu	Gly	Ile	Thr	Phe	Met	Ser	Leu	Met	Val	Asn	Thr	Cys	Tyr	170	175	180
Asp	Ile	Thr	Ala	Glu	Gly	Val	Pro	Phe	Ile	Pro	Tyr	Ala	Cys	Ala	185	190	195
Gly	Val	Gly	Ala	Asp	Leu	Ile	Asn	Val	Phe	Lys	Asp	Phe	Asn	Leu	200	205	210
Lys	Phe	Ser	Tyr	Gln	Gly	Lys	Ile	Gly	Ile	Ser	Tyr	Pro	Ile	Thr	215	220	225
Pro	Glu	Val	Ser	Ala	Phe	Ile	Gly	Gly	Tyr	Tyr	His	Gly	Val	Ile	230	235	240
Gly	Asn	Asn	Phe	Asn	Lys	Ile	Pro	Val	Ile	Thr	Pro	Val	Val	Leu	245	250	255
Glu	Gly	Ala	Pro	Gln	Thr	Thr	Ser	Ala	Leu	Val	Thr	Ile	Asp	Thr	260	265	270
Gly	Tyr	Phe	Gly	Gly	Glu	Val	Gly	Val	Arg	Phe	Thr	Phe			275	280	

<210> 11

<211> 280

<212> PRT

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* OMP-1C

<400> 11

Met	Asn	Cys	Lys	Lys	Phe	Phe	Ile	Thr	Thr	Ala	Leu	Ala	Leu	Pro	5	10	15
Met	Ser	Phe	Leu	Pro	Gly	Ile	Leu	Leu	Ser	Glu	Pro	Val	Gln	Asp	20	25	30
Asp	Ser	Val	Ser	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro	35	40	45
Ser	Ala	Ser	His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn	50	55	60

Pro	Thr	Val	Ala	Leu	Tyr	Gly	Leu	Lys	Gln	Asp	Trp	Asn	Gly	Val	
				65					70					75	
Ser	Ala	Ser	Ser	His	Ala	Asp	Ala	Asp	Phe	Asn	Asn	Lys	Gly	Tyr	
				80					85					90	
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala	
				95					100					105	
Ile	Gly	Tyr	Ser	Met	Gly	Gly	Pro	Arg	Ile	Glu	Phe	Glu	Val	Ser	
				110					115					120	
Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn	Gln	Gly	Gly	Asn	Tyr	Lys	Asn	
				125					130					135	
Asp	Ala	His	Arg	Tyr	Cys	Ala	Leu	Asp	Arg	Lys	Ala	Ser	Ser	Thr	
				140					145					150	
Asn	Ala	Thr	Ala	Ser	His	Tyr	Val	Leu	Leu	Lys	Asn	Glu	Gly	Leu	
				155					160					165	
Leu	Asp	Ile	Ser	Leu	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Val	Val	Ser	
				170					175					180	
Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Val	Gly	Thr	
				185					190					195	
Asp	Leu	Ile	Ser	Met	Phe	Glu	Ala	Ile	Asn	Pro	Lys	Ile	Ser	Tyr	
				200					205					210	
Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Asn	Pro	Glu	Ala	Ser	
				215					220					225	
Val	Phe	Val	Gly	Gly	His	Phe	His	Lys	Val	Ala	Gly	Asn	Glu	Phe	
				230					235					240	
Arg	Asp	Ile	Ser	Thr	Leu	Lys	Ala	Phe	Ala	Thr	Pro	Ser	Ser	Ala	
				245					250					255	
Ala	Thr	Pro	Asp	Leu	Ala	Thr	Val	Thr	Leu	Ser	Val	Cys	His	Phe	
				260					265					270	
Gly	Val	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe						
				275					280						

<210> 12
 <211> 286
 <212> PRT

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* OMP-1D

<400>	12	
Met Asn Cys Glu Lys Phe Phe Ile Thr Thr Ala Leu Thr Leu Leu		
	5	10 15
Met Ser Phe Leu Pro Gly Ile Ser Leu Ser Asp Pro Val Gln Asp		
	20	25 30
Asp Asn Ile Ser Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro		
	35	40 45
Ser Ala Ser His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn		
	50	55 60
Thr Thr Val Gly Val Phe Gly Ile Glu Gln Asp Trp Asp Arg Cys		
	65	70 75
Val Ile Ser Arg Thr Thr Leu Ser Asp Ile Phe Thr Val Pro Asn		
	80	85 90
Tyr Ser Phe Lys Tyr Glu Asn Asn Leu Phe Ser Gly Phe Ala Gly		
	95	100 105
Ala Ile Gly Tyr Ser Met Asp Gly Pro Arg Ile Glu Leu Glu Val		
	110	115 120
Ser Tyr Glu Ala Phe Asp Val Lys Asn Gln Gly Asn Asn Tyr Lys		
	125	130 135
Asn Glu Ala His Arg Tyr Tyr Ala Leu Ser His Leu Leu Gly Thr		
	140	145 150
Glu Thr Gln Ile Asp Gly Ala Gly Ser Ala Ser Val Phe Leu Ile		
	155	160 165
Asn Glu Gly Leu Leu Asp Lys Ser Phe Met Leu Asn Ala Cys Tyr		
	170	175 180
Asp Val Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala		
	185	190 195
Gly Ile Gly Ile Asp Leu Val Ser Met Phe Glu Ala Ile Asn Pro		
	200	205 210

Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Pro	Ile	Ser
				215					220					225
Pro	Glu	Ala	Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile
				230					235					240
Gly	Asn	Glu	Phe	Arg	Asp	Ile	Pro	Thr	Met	Ile	Pro	Ser	Glu	Ser
				245					250					255
Ala	Leu	Ala	Gly	Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Thr	Leu	Asp
				260					265					270
Val	Phe	Tyr	Phe	Gly	Ile	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe	Gln
				275					280					285

Leu

<210> 13
 <211> 278
 <212> PRT
 <213> *Ehrlichia chaffeensis*

<220>
 <223> amino acid sequence of *E. chaffeensis* OMP-1E

<400> 13														
Met	Asn	Cys	Lys	Lys	Phe	Phe	Ile	Thr	Thr	Ala	Leu	Val	Ser	Leu
				5					10					15
Met	Ser	Phe	Leu	Pro	Gly	Ile	Ser	Phe	Ser	Asp	Pro	Val	Gln	Gly
				20					25					30
Asp	Asn	Ile	Ser	Gly	Asn	Phe	Tyr	Val	Ser	Gly	Lys	Tyr	Met	Pro
				35					40					45
Ser	Ala	Ser	His	Phe	Gly	Met	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn
				50					55					60
Pro	Thr	Val	Ala	Leu	Tyr	Gly	Leu	Lys	Gln	Asp	Trp	Glu	Gly	Ile
				65					70					75
Ser	Ser	Ser	Ser	His	Asn	Asp	Asn	His	Phe	Asn	Asn	Lys	Gly	Tyr
				80					85					90
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala
				95					100					105

Ile Gly Tyr Ser Met Gly Gly Pro Arg Val Glu Phe Glu Val Ser		
	110	115 120
Tyr Glu Thr Phe Asp Val Lys Asn Gln Gly Asn Asn Tyr Lys Asn		
	125	130 135
Asp Ala His Arg Tyr Cys Ala Leu Gly Gln Gln Asp Asn Ser Gly		
	140	145 150
Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu Lys Ser Glu Gly Leu		
	155	160 165
Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr Asp Ile Ile Asn		
	170	175 180
Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly Val Gly Thr		
	185	190 195
Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile Ser Tyr		
	200	205 210
Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala Ser		
	215	220 225
Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe		
	230	235 240
Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr		
	245	250 255
Pro Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile		
	260	265 270
Glu Leu Gly Gly Arg Phe Asn Phe		
	275	

<210> 14

<211> 280

<212> PRT

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* OMP-1F

<400>	14														
Met	Asn	Cys	Lys	Lys	Phe	Phe	Ile	Thr	Thr	Thr	Leu	Val	Ser	Leu	
				5					10					15	
Met	Ser	Phe	Leu	Pro	Gly	Ile	Ser	Phe	Ser	Asp	Ala	Val	Gln	Asn	
				20					25					30	
Asp	Asn	Val	Gly	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Val	Pro	
				35					40					45	
Ser	Val	Ser	His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Gln	Glu	Arg	Asn	
				50					55					60	
Thr	Thr	Thr	Gly	Val	Phe	Gly	Leu	Lys	Gln	Asp	Trp	Asp	Gly	Ser	
				65					70					75	
Thr	Ile	Ser	Lys	Asn	Ser	Pro	Glu	Asn	Thr	Phe	Asn	Val	Pro	Asn	
				80					85					90	
Tyr	Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	
				95					100					105	
Ala	Val	Gly	Tyr	Leu	Met	Asn	Gly	Pro	Arg	Ile	Glu	Leu	Glu	Met	
				110					115					120	
Ser	Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn	Gln	Gly	Asn	Asn	Tyr	Lys	
				125					130					135	
Asn	Asp	Ala	His	Lys	Tyr	Tyr	Ala	Leu	Thr	His	Asn	Ser	Gly	Gly	
				140					145					150	
Lys	Leu	Ser	Asn	Ala	Gly	Asp	Lys	Phe	Val	Phe	Leu	Lys	Asn	Glu	
				155					160					165	
Gly	Leu	Leu	Asp	Ile	Ser	Leu	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Val	
				170					175					180	
Ile	Ser	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Val	
				185					190					195	
Gly	Thr	Asp	Leu	Ile	Ser	Met	Phe	Glu	Ala	Ile	Asn	Pro	Lys	Ile	
				200					205					210	
Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Ser	Pro	Glu	
				215					220					225	
Ala	Ser	Val	Phe	Val	Gly	Gly	His	Phe	His	Lys	Val	Ile	Gly	Asn	
				230					235					240	
Glu	Phe	Arg	Asp	Ile	Pro	Ala	Met	Ile	Pro	Ser	Thr	Ser	Thr	Leu	
				245					250					255	

Thr	Gly	Asn	His	Phe	Thr	Ile	Val	Thr	Leu	Ser	Val	Cys	His	Phe
				260					265					270
Gly	Val	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe					
				275					280					

<210> 15
 <211> 284
 <212> PRT
 <213> *Cowdria ruminantium*

<220>
 <223> amino acid sequence of *C. ruminantium* MAP-1

<400>				15										
Met	Asn	Cys	Lys	Lys	Ile	Phe	Ile	Thr	Ser	Thr	Leu	Ile	Ser	Leu
				5					10					15
Val	Ser	Phe	Leu	Pro	Gly	Val	Ser	Phe	Ser	Asp	Val	Ile	Gln	Glu
				20					25					30
Glu	Asn	Asn	Pro	Val	Gly	Ser	Val	Tyr	Ile	Ser	Ala	Lys	Tyr	Met
				35					40					45
Pro	Thr	Ala	Ser	His	Phe	Gly	Lys	Met	Ser	Ile	Lys	Glu	Asp	Ser
				50					55					60
Arg	Asp	Thr	Lys	Ala	Val	Phe	Gly	Leu	Lys	Lys	Asp	Trp	Asp	Gly
				65					70					75
Val	Lys	Thr	Pro	Ser	Gly	Asn	Thr	Asn	Ser	Ile	Phe	Thr	Glu	Lys
				80					85					90
Asp	Tyr	Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala
				95					100					105
Gly	Ala	Val	Gly	Tyr	Ser	Met	Asn	Gly	Pro	Arg	Ile	Glu	Phe	Glu
				110					115					120
Val	Ser	Tyr	Glu	Thr	Phe	Asp	Val	Arg	Asn	Pro	Gly	Gly	Asn	Tyr
				125					130					135
Lys	Asn	Asp	Ala	His	Met	Tyr	Cys	Ala	Leu	Asp	Thr	Ala	Ser	Ser
				140					145					150

Ser Thr Ala Gly Ala Thr Thr Ser Val Met Val Lys Asn Glu Asn		
	155	160 165
Leu Thr Asp Ile Ser Leu Met Leu Asn Ala Cys Tyr Asp Ile Met		
	170	175 180
Leu Asp Gly Met Pro Val Ser Pro Tyr Val Cys Ala Gly Ile Gly		
	185	190 195
Thr Asp Leu Val Ser Val Ile Asn Ala Thr Asn Pro Lys Leu Ser		
	200	205 210
Tyr Gln Gly Lys Leu Gly Ile Ser Tyr Ser Ile Asn Pro Glu Ala		
	215	220 225
Ser Ile Phe Ile Gly Gly His Phe His Arg Val Ile Gly Asn Glu		
	230	235 240
Phe Lys Asp Ile Ala Thr Ser Lys Val Phe Thr Ser Ser Gly Asn		
	245	250 255
Ala Ser Ser Ala Val Ser Pro Gly Phe Ala Ser Ala Ile Leu Asp		
	260	265 270
Val Cys His Phe Gly Ile Glu Ile Gly Gly Arg Phe Val Phe		
	275	280

<210> 16

<211> 20

<212> DNA

<213> artificial sequence

<220>

<221> primer_bind

<222> nucleotides 313-332 of *C. ruminantium* MAP-1,
also nucleotides 307-326 of *E. chaffeensis* P28

<223> forward primer 793 for PCR

<400> 16

gcaggagctg ttggttactc

20

<210>	17	
<211>	21	
<212>	DNA	
<213>	artificial sequence	
<220>		
<221>	primer_bind	
<222>	nucleotides 823-843 of <i>C. ruminantium</i> MAP-1,	
	also nucleotides 814-834 of <i>E. chaffeensis</i> P28	
<223>	reverse primer 1330 for PCR	
<400>	17	
ccttcctcca agttctatgc c		21
<210>	18	
<211>	24	
<212>	DNA	
<213>	artificial sequence	
<220>		
<221>	primer_bind	
<223>	primer 46f, specific for p28-5 gene	
<400>	18	
atatacttcc tacctaattgt ctca		24
<210>	19	
<211>	20	
<212>	DNA	
<213>	artificial sequence	
<220>		
<221>	primer_bind	

<223> primer used for sequencing 28-kDa protein
 genes in *E. canis*

<400> 19
 agtgcagagt cttcggtttc 20

<210> 20
 <211> 18
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <223> primer used for sequencing 28-kDa protein
 genes in *E. canis*

<400> 20
 gttacttgcg gaggacat 18

<210> 21
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <222> nucleotides 687-710 of *E. canis* p28-7
 <223> primer 394 for PCR

<400> 21
 gcatttccac aggatcatag gtaa 24

<210>	22	
<211>	24	
<212>	DNA	
<213>	artificial sequence	
<220>		
<221>	primer_bind	
<222>	nucleotides 710-687 of <i>E. canis p28-7</i>	
<223>	primer 394C for PCR	
<400>	22	
ttacctatga tcctgtggaa atgc		24
<210>	23	
<211>	20	
<212>	DNA	
<213>	artificial sequence	5
<220>		
<221>	primer_bind	
<223>	primer 793C which anneals to a region with <i>E. canis p28-7</i> , used to amplify the intergenic region between gene <i>p28-6</i> and <i>p28-7</i>	
<400>	23	
gagtaaccaa cagctcctgc		20
<210>	24	
<211>	24	
<212>	DNA	
<213>	artificial sequence	
<220>		
<221>	primer_bind	

<222>
 <223> primer EC28OM-F complementary to noncoding regions
 adjacent to the open reading frame of *p28-7*

<400> 24
 tctacttttgc acttccacta ttgt 24

<210> 25
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <222>
 <223> primer EC28OM-R complementary to noncoding regions
 adjacent to the open reading frame of *p28-7*

<400> 25
 attctttttgc cactatttttt cttt 24

<210> 26
 <211> 25
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <223> primer *ECaSA3-2* corresponding to regions within
p28-6, used to amplify the intergenic region NC3
 between gene *p28-6* and *p28-7*

<400> 26
 ctaggattag gttatagtat aagtt 25

<210> 27
 <211> 23
 <212> PRT
 <213> *Ehrlichia canis*

<220>
 <221> PEPTIDE
 <223> a predicted N-terminal signal peptide of p28-7
 and p28-6

<400> 27
 Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Met Ser Leu
 5 10 15
 Met Tyr Tyr Ala Pro Ser Ile Ser
 20

<210> 28
 <211> 25
 <212> PRT
 <213> *Ehrlichia chaffeensis*

<220>
 <223> amino acid sequence of N-terminal signal peptide of
E. chaffeensis P28

<400> 28
 Met Asn Tyr Lys Lys Ile Leu Ile Thr Ser Ala Leu Ile Ser Leu
 5 10 15
 Ile Ser Ser Leu Pro Gly Val Ser Phe Ser
 20 25

<210> 29
 <211> 26

<212> PRT

<213> *Ehrlichia canis*

<220>

<223> amino acid sequence of putative cleavage site of
p28-7

<400> 29

Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Ile Ser Leu

5 10 15

Met Tyr Ser Ile Pro Ser Ile Ser Ser Phe Ser

20 25

<210> 30

<211> 299

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic
noncoding region 1 (28NC1)

<400> 30

taatacttct attgtacatg ttaaaaatag tactagtttg cttctgtggt 50

ttataaacgc aagagagaaa tagttagtaa taaattagaa agttaaatat 100

tagaaaagtc atatgttttt cattgtcatt gatactcaac taaaagtagt 150

ataaatgtta cttattaata attttacgta gtatattaaa tttcccttac 200

aaaagccact agtatatttat actaaaagct atactttggc ttgtatttaa 250

tttgtatttt tactactggt aatttacttt cactgtttct ggtgtaaat 299

<210> 31

<211> 345

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic noncoding
region 2 (28NC2)

<400> 31
taatttcgtg gtacacatat cacgaagcta aaattgtttt tttatctctg 50
ctgtatacaa gagaaaaaat agtagtgaaa attacctaac aatatgacag 100
tacaagttta ccaagcttat tctcacaaaa cttcttgtgt cttttatctc 150
tttacaatga aatgtacact tagcttcact actgtagagt gtgtttatca 200
atgctttgtt tattaatact ctacataata tgtaaattt ttcttacaaa 250
actcactagt aatttatact agaatatata ttctgacttg tatttgcttt 300
atacttccac tattgttaat ttattttcac tatttttaggt gtaat 345

<210> 32

<211> 345

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic
noncoding region 3 (28NC3)

<400> 32
tgatttttatt gttgccacat attaaaaatg atctaaactt gtttttatta 50
ttgctacata caaaaaaaag aaaaatagtg gcaaaagaat gtagcaataa 100
gagggggggg ggggactaaa ttaccttct attcttctaa tattctttac 150
tatattcaaa tagcacaact caatgcttcc aggaaaatat gtttctaata 200
ttttatttat taccaatcct tatataatat attaaatttc tcttacaaaa 250
atctctaaty ttttatactt aatatatata ttctggcttg tatttacttt 300
gcacttccac tattgttaat ttattttcac tatttttaggt gtaat 345

<210> 33

<211> 355

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic
noncoding region 4 (28NC4)

<400> 33
taatttttatt gttgccacat attaaaaatg atctaaactt gttttttawta 50
ttgctacata caaaaaaaga aaaatagtgg caaaagaatg tagcaataag 100
agggggggggg gggaccaaatt ttatcttcta tgcttcccaa gtttttttcyc 150
gctattttatg acttaaacaa cagaaggtaa tatcctcacg gaaaacttat 200
cttcaaatat tttatttatt accaatctta tataatatat taaatttctc 250
ttacaaaaat cactagtatt ttataccaaa atatatttc tgacttgctt 300
ttcttctgca cttctactat ttttaattta tttgtcacta ttaggttata 350
ataaw 355

<210> 34

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> primer p28-5-818f

<400> 34
ttaaacatat gccacttcgg acta 24

<210> 35

<211> 28

<212> DNA

<213> artificial sequence

<220>

<223> primer 1191

<400> 35
tatgatcgtg taaaattgct gtgagtat 28

<210> 36
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> primer ECa28-75C

<400> 36
tactggcacg tgctggacta 20

<210> 37
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> primer ECa5'-1600

<400> 37
caccaataaa tgcagagact tc 22

<210> 38
<211> 26
<212> DNA
<213> artificial sequence

<220>
<223> primer 3125

<400> 38
aatccatcat ttctcattac agtgtg 26

<210> 39

<211> 879

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of *E. canis* p28-1

<400> 39
atgaataata aactcaaatt tactataata aacacagtat tagtatgctt 50
attgtcatta cctaataatat cttcctcaaa ggccataaac aataacgcta 100
aaaagtacta cggattatat atcagtggac aatataaacc cagtgtttct 150
gttttcagta atttttcagt taaagaaacc aatgtcataa ctaaaaacct 200
tatagcttta aaaaaagatg ttgactctat tgaaaccaag actgatgcc 250
gtgtaggtat tagtaacca tcaaatttta ctatccccta tacagctgta 300
tttcaagata attctgtcaa tttcaatgga actattgggtt acacctttgc 350
tgaaggatca agagttgaaa tagaagggtc ttatgaggaa tttgatgtta 400
aaaacctgg aggctataca ctaagtgatg cctatcgcta ttttgcat 450
gcacgtgaaa tgaaaggtaa tagttttaca cctaaagaaa aagttttctaa 500
tagtatTTTTT cacactgtaa tgagaaatga tggattatct ataatatctg 550
ttatagtaaa tgtttgctac gatttctctt tgaacaattt gtcaatatcg 600
ccttacatat gtggaggagc aggggtagat gctatagaat tcttcgatgt 650
attacacatt aagtttgc atcaaagcaa gctaggtatt gcttattctc 700
taccatctaa cattagtctc tttgctagtt tatattacca taaagtaatg 750
ggcaatcaat ttaaaaattt aaatgtccaa catgttgctg aacttgcaag 800
tatacctaaa attacatccg cagttgctac acttaatat gggtattttg 850
gaggtgaaat tgggtgcaaga ttgacattt 879

<210> 40

<211> 293

<212> PRT

<213> *Ehrlichia canis*

<220>

<223> amino acid sequence of *E. canis* p28-1 protein

<400> 40

Met	Asn	Asn	Lys	Leu	Lys	Phe	Thr	Ile	Ile	Asn	Thr	Val	Leu	Val	
				5					10					15	
Cys	Leu	Leu	Ser	Leu	Pro	Asn	Ile	Ser	Ser	Ser	Lys	Ala	Ile	Asn	
				20					25					30	
Asn	Asn	Ala	Lys	Lys	Tyr	Tyr	Gly	Leu	Tyr	Ile	Ser	Gly	Gln	Tyr	
				35					40					45	
Lys	Pro	Ser	Val	Ser	Val	Phe	Ser	Asn	Phe	Ser	Val	Lys	Glu	Thr	
				50					55					60	
Asn	Val	Ile	Thr	Lys	Asn	Leu	Ile	Ala	Leu	Lys	Lys	Asp	Val	Asp	
				65					70					75	
Ser	Ile	Glu	Thr	Lys	Thr	Asp	Ala	Ser	Val	Gly	Ile	Ser	Asn	Pro	
				80					85					90	
Ser	Asn	Phe	Thr	Ile	Pro	Tyr	Thr	Ala	Val	Phe	Gln	Asp	Asn	Ser	
				95					100					105	
Val	Asn	Phe	Asn	Gly	Thr	Ile	Gly	Tyr	Thr	Phe	Ala	Glu	Gly	Thr	
				110					115					120	
Arg	Val	Glu	Ile	Glu	Gly	Ser	Tyr	Glu	Glu	Phe	Asp	Val	Lys	Asn	
				125					130					135	
Pro	Gly	Gly	Tyr	Thr	Leu	Ser	Asp	Ala	Tyr	Arg	Tyr	Phe	Ala	Leu	
				140					145					150	
Ala	Arg	Glu	Met	Lys	Gly	Asn	Ser	Phe	Thr	Pro	Lys	Glu	Lys	Val	
				155					160					165	
Ser	Asn	Ser	Ile	Phe	His	Thr	Val	Met	Arg	Asn	Asp	Gly	Leu	Ser	
				170					175					180	
Ile	Ile	Ser	Val	Ile	Val	Asn	Val	Cys	Tyr	Asp	Phe	Ser	Leu	Asn	
				185					190					195	
Asn	Leu	Ser	Ile	Ser	Pro	Tyr	Ile	Cys	Gly	Gly	Ala	Gly	Val	Asp	
				200					205					210	
Ala	Ile	Glu	Phe	Phe	Asp	Val	Leu	His	Ile	Lys	Phe	Ala	Tyr	Gln	
				215					220					225	
Ser	Lys	Leu	Gly	Ile	Ala	Tyr	Ser	Leu	Pro	Ser	Asn	Ile	Ser	Leu	
				230					235					240	

Phe	Ala	Ser	Leu	Tyr	Tyr	His	Lys	Val	Met	Gly	Asn	Gln	Phe	Lys
			245						250					255
Asn	Leu	Asn	Val	Gln	His	Val	Ala	Glu	Leu	Ala	Ser	Ile	Pro	Lys
			260						265					270
Ile	Thr	Ser	Ala	Val	Ala	Thr	Leu	Asn	Ile	Gly	Tyr	Phe	Gly	Gly
			275						280					285
Glu	Ile	Gly	Ala	Arg	Leu	Thr	Phe							
			290				293							

<210> 41

<211> 840

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of *E. canis* p28-2

<400> 41

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aatcttacca tatcagtctt ttgcagatcc ttagagttca agaactaatg 100
ataacaaaga aggccttctac attagtgc aaagacaatcc aagtatatca 150
cactttagaa aattctctgc tgaagaaact cctattaatg gaacaaattc 200
tctcactaaa aaagtttttcg gactaaagaa agatgggtgat ataacaaaaa 250
aagacgattt tacaagagta gctccaggca ttgattttca aaataactta 300
atatcaggat ttccaggaag tattgggttac tctatggacg gaccaagaat 350
agaacttgaa gctgcatatc aacaatttaa tccaaaaaac accgataaca 400
atgataactga taatgggtgaa tactataaac attttgcatt atctcgtaaa 450
gatgcaatgg aagatcagca atatgtagta cttaaaaatg acggcataac 500
ttttatgtca ttgatgggta atacttgcta tgacattaca gctgaaggag 550
tatctttcgt accatatgca tgtgcaggta taggagcaga tcttatcact 600
atTTTTaaag acctcaatct aaaatttgct taccaaggaa aaataggtat 650
tagttaccct atcacaccag aagtctctgc atttattggt ggatactacc 700
atggcgttat tggtaataaaa ttgagaaga tacctgtaat aactcctgta 750
gtattaaatg atgctcctca aaccacatct gcttcagtaa ctcttgacgt 800
tggatacttt ggcggagaaa ttggaatgag gttcaccttc 840

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<210> 42
 <211> 280
 <212> PRT
 <213> *Ehrlichia canis*

 <220>
 <223> amino acid sequence of *E. canis* p28-2 protein

<400> 42
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 Met Ser Ile Leu Pro Tyr Gln Ser Phe Ala Asp Pro Val Gly Ser
 20 25 30
 Arg Thr Asn Asp Asn Lys Glu Gly Phe Tyr Ile Ser Ala Lys Tyr
 35 40 45
 Asn Pro Ser Ile Ser His Phe Arg Lys Phe Ser Ala Glu Glu Thr
 50 55 60
 Pro Ile Asn Gly Thr Asn Ser Leu Thr Lys Lys Val Phe Gly Leu
 65 70 75
 Lys Lys Asp Gly Asp Ile Thr Lys Lys Asp Asp Phe Thr Arg Val
 80 85 90
 Ala Pro Gly Ile Asp Phe Gln Asn Asn Leu Ile Ser Gly Phe Ser
 95 100 105
 Gly Ser Ile Gly Tyr Ser Met Asp Gly Pro Arg Ile Glu Leu Glu
 110 115 120
 Ala Ala Tyr Gln Gln Phe Asn Pro Lys Asn Thr Asp Asn Asn Asp
 125 130 135
 Thr Asp Asn Gly Glu Tyr Tyr Lys His Phe Ala Leu Ser Arg Lys
 140 145 150
 Asp Ala Met Glu Asp Gln Gln Tyr Val Val Leu Lys Asn Asp Gly
 155 160 165
 Ile Thr Phe Met Ser Leu Met Val Asn Thr Cys Tyr Asp Ile Thr
 170 175 180
 Ala Glu Gly Val Ser Phe Val Pro Tyr Ala Cys Ala Gly Ile Gly
 185 190 195

Ala Asp Leu Ile Thr Ile Phe Lys Asp Leu Asn Leu Lys Phe Ala		
	200	210
Tyr Gln Gly Lys Ile Gly Ile Ser Tyr Pro Ile Thr Pro Glu Val		
	215	225
Ser Ala Phe Ile Gly Gly Tyr Tyr His Gly Val Ile Gly Asn Lys		
	230	240
Phe Glu Lys Ile Pro Val Ile Thr Pro Val Val Leu Asn Asp Ala		
	245	255
Pro Gln Thr Thr Ser Ala Ser Val Thr Leu Asp Val Gly Tyr Phe		
	260	270
Gly Gly Glu Ile Gly Met Arg Phe Thr Phe		
	275	280

<210> 43
 <211> 828
 <212> DNA
 <213> *Ehrlichia canis*

<220>
 <223> nucleic acid sequence of *E. canis* p28-3

<400> 43
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 caggaaactt ttacattatt ggaaaatatg taccaagtat ttcacattttt 150
 gggaactttt cagctaaaga agaaaaaac acaacaactg gaattttttgg 200
 attaaaagaa tcatggactg gtggtatcat ccttgataaa gaacatgcag 250
 cttttaatat cccaaattat tcattttaaat atgaaaataa tccatttttta 300
 ggatttgcag gggtaattgg ctattcaata ggtagtccaa gaatagaatt 350
 tgaagtatca tacgagacat tcgatgtaca aaatccagga gataagttta 400
 acaatgatgc acataagtat tgtgctttat ccaatgattc cagtaaaaca 450
 atgaaaagtg gtaaatcgt ttttctcaaa aatgaaggat taagtgcacat 500
 atcactcatg ttaaatgtat gttatgatat aataaacaaga agaatgcctt 550
 tttcacctta catatgtgca ggcattggta ctgacttaat attcatgttt 600
 gacgctataa accataaagc tgcttatcaa ggaaaattag gttttaatta 650

tccaataagc ccagaagcta acatttctat ggggtgtgcac tttcacaaag 700
 taacaaacaa cgagtttaga gttcctgttc tattaactgc tggaggactc 750
 gctccagata atctatttgc aatagtaaag ttgagtatat gtcattttgg 800
 gttagaattt gggtacaggg tcagtttt 828

<210> 44

<211> 276

<212> PRT

<213> *Ehrlichia canis*

<220>

<223> amino acid sequence of *E. canis* p28-3 protein

<400> 44

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Thr	Ile	Leu	Leu	Pro	Gly	Ile	Ser	Phe	Ser	Lys	Pro	Ile	His	Glu	
				20					25					30	
Asn	Asn	Thr	Thr	Gly	Asn	Phe	Tyr	Ile	Ile	Gly	Lys	Tyr	Val	Pro	
				35					40					45	
Ser	Ile	Ser	His	Phe	Gly	Asn	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn	
				50					55					60	
Thr	Thr	Thr	Gly	Ile	Phe	Gly	Leu	Lys	Glu	Ser	Trp	Thr	Gly	Gly	
				65					70					75	
Ile	Ile	Leu	Asp	Lys	Glu	His	Ala	Ala	Phe	Asn	Ile	Pro	Asn	Tyr	
				80					85					90	
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Val	
				95					100					105	
Ile	Gly	Tyr	Ser	Ile	Gly	Ser	Pro	Arg	Ile	Glu	Phe	Glu	Val	Ser	
				110					115					120	
Tyr	Glu	Thr	Phe	Asp	Val	Gln	Asn	Pro	Gly	Asp	Lys	Phe	Asn	Asn	
				125					130					135	
Asp	Ala	His	Lys	Tyr	Cys	Ala	Leu	Ser	Asn	Asp	Ser	Ser	Lys	Thr	
				140					145					150	

Met	Lys	Ser	Gly	Lys	Phe	Val	Phe	Leu	Lys	Asn	Glu	Gly	Leu	Ser	155	160	165
Asp	Ile	Ser	Leu	Met	Leu	Asn	Val	Cys	Tyr	Asp	Ile	Ile	Asn	Lys	170	175	180
Arg	Met	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Ile	Gly	Thr	Asp	185	190	195
Leu	Ile	Phe	Met	Phe	Asp	Ala	Ile	Asn	His	Lys	Ala	Ala	Tyr	Gln	200	205	210
Gly	Lys	Leu	Gly	Phe	Asn	Tyr	Pro	Ile	Ser	Pro	Glu	Ala	Asn	Ile	215	220	225
Ser	Met	Gly	Val	His	Phe	His	Lys	Val	Thr	Asn	Asn	Glu	Phe	Arg	230	235	240
Val	Pro	Val	Leu	Leu	Thr	Ala	Gly	Gly	Leu	Ala	Pro	Asp	Asn	Leu	245	250	255
Phe	Ala	Ile	Val	Lys	Leu	Ser	Ile	Cys	His	Phe	Gly	Leu	Glu	Phe	260	265	270
Gly	Tyr	Arg	Val	Ser	Phe										275		

<210> 45
 <211> 813
 <212> DNA
 <213> *Ehrlichia canis*

<220>
 <223> nucleic acid sequence of *E. canis* p28-9

<400> 45
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 gaggacttta tataggtagt cagtataaag ttggtattcc caatttttagt 150
 aatttttcag ctgaagaaac aattcctggt attacaaaaa agatttttgc 200
 gttaggtctt gataagtctg agataaatac tcacagcaat tttacacgat 250
 catatgaccc tacttatgca agcagttttg cagggttttag tggtatcatt 300
 ggatattatg ttaatgactt tagggtagaa tttgaagggt cttatgagaa 350

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ttttgaacct gaaagacaat ggtaccctga gaatagccaa agctacaaat 400
tttttgcttt gtctcgaaat gctacaaata gtgataataa gtttatagta 450
ctagagaata acggcgttgt tgacaagtct cttaatgtaa atgtttgtta 500
tgatattgct agtggttagta ttccttttagc accttatatg tgtgctggtg 550
ttggtgcaga ttatataaag ttttttaggta tatcattgcc taagttttct 600
tatcaagtta agtttggtgt caactaccct ctaaagtgtta atactatggt 650
gtttggtggg ggttattacc ataagggtgt aggtgatagg catgagagag 700
tagaaatagc ttaccatcct actgcattat ctgacgttcc tagaactact 750
tcagcttctg ctactttaaa tactgattat tttggttggg agattggatt 800
tagatttgcg cta                                     813

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<210>      46
<211>      271
<212>      PRT
<213>      Ehrlichia canis

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<220>
<223>      amino acid sequence of E. canis p28-9 protein

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<400>      46
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Val Phe Phe Leu Ser Asp Gly Ala Phe Ser Asp Ala Asn Phe Ser
              20                      25                      30
Glu Gly Arg Arg Gly Leu Tyr Ile Gly Ser Gln Tyr Lys Val Gly
              35                      40                      45
Ile Pro Asn Phe Ser Asn Phe Ser Ala Glu Glu Thr Ile Pro Gly
              50                      55                      60
Ile Thr Lys Lys Ile Phe Ala Leu Gly Leu Asp Lys Ser Glu Ile
              65                      70                      75
Asn Thr His Ser Asn Phe Thr Arg Ser Tyr Asp Pro Thr Tyr Ala
              80                      85                      90
Ser Ser Phe Ala Gly Phe Ser Gly Ile Ile Gly Tyr Tyr Val Asn
              95                      100                     105

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Asp	Phe	Arg	Val	Glu	Phe	Glu	Gly	Ser	Tyr	Glu	Asn	Phe	Glu	Pro			
				110					115					120			
Glu	Arg	Gln	Trp	Tyr	Pro	Glu	Asn	Ser	Gln	Ser	Tyr	Lys	Phe	Phe			
				125					130					135			
Ala	Leu	Ser	Arg	Asn	Ala	Thr	Asn	Ser	Asp	Asn	Lys	Phe	Ile	Val			
				140					145					150			
Leu	Glu	Asn	Asn	Gly	Val	Val	Asp	Lys	Ser	Leu	Asn	Val	Asn	Val			
				155					160					165			
Cys	Tyr	Asp	Ile	Ala	Ser	Gly	Ser	Ile	Pro	Leu	Ala	Pro	Tyr	Met			
				170					175					180			
Cys	Ala	Gly	Val	Gly	Ala	Asp	Tyr	Ile	Lys	Phe	Leu	Gly	Ile	Ser			
				185					190					195			
Leu	Pro	Lys	Phe	Ser	Tyr	Gln	Val	Lys	Phe	Gly	Val	Asn	Tyr	Pro			
				200					205					210			
Leu	Asn	Val	Asn	Thr	Met	Leu	Phe	Gly	Gly	Gly	Tyr	Tyr	His	Lys			
				215					220					225			
Val	Val	Gly	Asp	Arg	His	Glu	Arg	Val	Glu	Ile	Ala	Tyr	His	Pro			
				230					235					240			
Thr	Ala	Leu	Ser	Asp	Val	Pro	Arg	Thr	Thr	Ser	Ala	Ser	Ala	Thr			
				245					250					255			
Leu	Asn	Thr	Asp	Tyr	Phe	Gly	Trp	Glu	Ile	Gly	Phe	Arg	Phe	Ala			
				260					265					270			
Leu																	
271																	